```
        10                          30                          50
CACGCGTCCGCGGGCGCGGCCGGAGAACCCCGCAATCTTTGCGCCCACAAAATACACCGA
        70                          90                          110
CGATGCCCGATCTACTTTAAGGGCTGAAACCCACGGGCCTGAGAGACTATAAGAGCGTTC
        130                         150                         170
CCTACCGCCATGGAACAACGGGGACAGAACGCCCCGGCCGCTTCGGGGGCCCGGAAAAGG
          M  E  Q  R  G  Q  N  A  P  A  A  S  G  A  R  K  R
        190                         210                         230
CACGGCCCAGGACCCAGGGAGGCGCGGGGAGCCAGGCCTGGCCCCCGGGTCCCCAAGACC
 H  G  P  G  P  R  E  A  R  G  A  R  P  G  P  R  V  P  K  T
        250                         270                         290
CTTGTGCTCGTTGTCGCCGCGGTCCTGCTGTTGGTCTCAGCTGAGTCTGCTCTGATCACC
 L  V  L  V  V  A  A  V  L  L  L  V  S  A  E  S  A  L  I  T
        310                         330                         350
CAACAAGACCTAGCTCCCCAGCAGAGAGCGGCCCCACAACAAAAGAGGTCCAGCCCCTCA
 Q  Q  D  L  A  P  Q  Q  R  A  A  P  Q  Q  K  R  S  S  P  S
        370                         390                         410
GAGGGATTGTGTCCACCTGGACACCATATCTCAGAAGACGGTAGAGATTGCATCTCCTGC
 E  G  L  C  P  P  G  H  H  I  S  E  D  G  R  D  C  I  S  C
        430                         450                         470
AAATATGGACAGGACTATAGCACTCACTGGAATGACCTCCTTTTCTGCTTGCGCTGCACC
 K  Y  G  Q  D  Y  S  T  H  W  N  D  L  L  F  C  L  R  C  T
        490                         510                         530
AGGTGTGATTCAGGTGAAGTGGAGCTAAGTCCCTGCACCACGACCAGAAACACAGTGTGT
 R  C  D  S  G  E  V  E  L  S  P  C  T  T  T  R  N  T  V  C
        550                         570                         590
CAGTGCGAAGAAGGCACCTTCCGGGAAGAAGATTCTCCTGAGATGTGCCGGAAGTGCCGC
 Q  C  E  E  G  T  F  R  E  E  D  S  P  E  M  C  R  K  C  R
        610                         630                         650
ACAGGGTGTCCCAGAGGGATGGTCAAGGTCGGTGATTGTACACCCTGGAGTGACATCGAA
 T  G  C  P  R  G  M  V  K  V  G  D  C  T  P  W  S  D  I  E
        670                         690                         710
TGTGTCCACAAAGAATCAGGCATCATCATAGGAGTCACAGTTGCAGCCGTAGTCTTGATT
 C  V  H  K  E  S  G  I  I  I  G  V  T  V  A  A  V  V  L  I
        730                         750                         770
GTGGCTGTGTTTGTTTGCAAGTCTTTACTGTGGAAGAAAGTCCTTCCTTACCTGAAAGGC
 V  A  V  F  V  C  K  S  L  L  W  K  K  V  L  P  Y  L  K  G
        790                         810                         830
ATCTGCTCAGGTGGTGGTGGGGACCCTGAGCGTGTGGACAGAAGCTCACAACGACCTGGG
 I  C  S  G  G  G  G  D  P  E  R  V  D  R  S  S  Q  R  P  G
```

FIG.1A

850 870 890
GCTGAGGACAATGTCCTCAATGAGATCGTGAGTATCTTGCAGCCCACCCAGGTCCCTGAG
A E D N V L N E I V S I L Q P T Q V P E

910 930 950
CAGGAAATGGAAGTCCAGGAGCCAGCAGAGCCAACAGGTGTCAACATGTTGTCCCCCGGG
Q E M E V Q E P A E P T G V N M L S P G

970 990 1010
GAGTCAGAGCATCTGCTGGAACCGGCAGAAGCTGAAAGGTCTCAGAGGAGGAGGCTGCTG
E S E H L L E P A E A E R S Q R R R L L

1030 1050 1070
GTTCCAGCAAATGAAGGTGATCCCACTGAGACTCTGAGACAGTGCTTCGATGACTTTGCA
V P A N E G D P T E T L R Q C F D D F A

1090 1110 1130
GACTTGGTGCCCTTTGACTCCTGGGAGCCGCTCATGAGGAAGTTGGGCCTCATGGACAAT
D L V P F D S W E P L M R K L G L M D N

1150 1170 1190
GAGATAAAGGTGGCTAAAGCTGAGGCAGCGGGCCACAGGGACACCTTGTACACGATGCTG
E I K V A K A E A A G H R D T L Y T M L

1210 1230 1250
ATAAAGTGGGTCAACAAAACCGGGCGAGATGCCTCTGTCCACACCCTGCTGGATGCCTTG
I K W V N K T G R D A S V H T L L D A L

1270 1290 1310
GAGACGCTGGGAGAGAGACTTGCCAAGCAGAAGATTGAGGACCACTTGTTGAGCTCTGGA
E T L G E R L A K Q K I E D H L L S S G

1330 1350 1370
AAGTTCATGTATCTAGAAGGTAATGCAGACTCTGCCATGTCCTAAGTGTGATTCTCTTCA
K F M Y L E G N A D S A M S *

1390 1410 1430
GGAAGTGAGACCTTCCCTGGTTTACCTTTTTCTGGAAAAAGCCCAACTGGACTCCAGTC

1450 1470 1490
AGTAGGAAAGTGCCACAATTGTCACATGACCGGTACTGGAAGAAACTCTCCCATCCAACA

1510 1530 1550
TCACCCAGTGGATGGAACATCCTGTAACTTTTCACTGCACTTGGCATTATTTTTATAAGC

1570 1590
TGAATGTGATAATAAGGACACTATGGAAAAAAAAAAAAAA

FIG.1B

```
1   M - L G - - - - - - - - - - - - - - - - - - - - - - - - - - - I W T L L P L V L   h Fas protein
1   M G L S - - - - - - - - - - - - - - - - - - - - - - - - - - - T V P D L L L P L   h TNFR I Protein
1   M E Q R - - - - - - - - - - - - - - - - - - - - - - - - - - - P R G C A A V A A   DR3 protein
1   M E Q R G Q N A P A A S G A R K R H G P G P R E A R G A R P G P R V P K T L V L   HLYBX88XXprotein

13  T S V A R L S S K S V N A Q V T D I N S K G L E L R K T V T T V E T Q N L E G L   h Fas protein
14  V L L E L L V G I Y P S G V I G L V P H L G D R E K R D S V C P Q G K Y I H - -   h TNFR I Protein
14  A L L L V L L G A R A Q G - - - - - - - - G T R S P R - C D C A - G D F - H - -   DR3 protein
41  V V A A V L L L V S A E S A L I T Q Q D L A P Q Q R A A P Q Q K R S S P S E G L   HLYBX88XXprotein

53  H H D G Q F C H K P C P P G E R K A R D C T V N G D E P D C V P C Q E G K E Y T   h Fas protein
52  P Q N N S I C C T K C H K G T Y L Y N D C P G P G Q D T D C R E C E S G S F T A   h TNFR I Protein
41  K K I G L F C C R G C P A G H Y L K A P C T E P C G N S T C L V C P Q D T F L A   DR3 protein
81  - - - - - - - - - - C P P G H H I S E D - - - - - - G R D C I S C K Y G Q D Y S   HLYBX88XXprotein

93  D K A H F S S K C R R C R L C D E G H G L E V E I N C T R T Q N T K C R C K P N   h Fas protein
92  S E N H L R - H C L S C S K C R K E M G Q V E I S S C T V D R D T V C G C R K N   h TNFR I Protein
81  W E N H H N S E C A R C Q A C D E Q A S Q V A L E N C S A V A D T R C G C K P G   DR3 protein
105 T H W N D L L F C L R C T R C D - - S G E V E L S P C T T T R N T V C Q C E E G   HLYBX88XXprotein

133 F F - - - - - - - - - - C N S T V - - - C E H C D P C T K - - - - - - - - - - -   h Fas protein
131 Q Y R H Y W S E N L F Q C - - - - - F N C S L C L N - G T V H - - - - L S C Q E   h TNFR I Protein
121 W F V E C - - - Q V S Q C V S S S P F Y C Q P C L D C G A L H R H T R L L C S R   DR3 protein
143 T F R E - - - - - - - - - - E D S P E M C R K C - - - - - - - - - - R T G C P R   HLYBX88XXprotein
```

FIG.2A

```
149 - - - - - - - C E H G I I - - - K E C - - - - - - - - T L T S N T K C K E - - - h Fas protein
161 K Q N T V C T C H A G F F L R E N E C V S C S N C K K S L E C T K L C L P Q I E h TNFR I Protein
158 R D T D C G T C L P G F Y E H G D G C V S C P T S T L G - S C P E R C A A V C G DR3 protein
163 G M V K V G D C T P - - - W S D I E C V - - - - - - - - - - - H K E S G I I I G HLYBX88XXprotein

168 - - - - - E G S R S N L G W - - - - - - - L C L L - L L P I P L I V - - - - - W h Fas protein
201 N V K G T E D S G T T V L L P L V I F F G L C L L S L L F I G L M Y R Y Q R - W h TNFR I Protein
197 W R Q - - - - - - - - M F W V Q V L L A G L V V P L L L G A T L T Y T Y R H C W DR3 protein
189 - - - - - - V T V A A V V L I V A V F - - V C K S L L W K K V L P Y L K G I C S HLYBX88XXprotein

190 V K R K E V Q K T C R K H R K E N Q G S H E S - - - - - - - - - - - - - - - - - h Fas protein
240 - K S K L Y S I V C G K S T P E K E G E L E G T T T K P L A P N P S F S P T P G h TNFR I Protein
229 - P H K P L - V T A D E A G M E A L T P P P A T H L S P L D S A H T L L A P P D DR3 protein
221 - - - - - - G G G G D P E R V D R S S Q R P G A E D N V L N E I V S I L Q P T Q HLYBX88XXprotein

213 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - h Fas protein
279 F T P T L G F S P V P S S T F T S S S T Y T P G D - C P N F A A P R R E V A P P h TNFR I Protein
267 S S E K I C T V Q L V G N S W T P G Y P E T Q E A L C P Q V T W S W D Q L - - P DR3 protein
255 V P E Q E M E V Q E P A E - - - - - - P T G V N M L S P G - - - E S E H L - - - HLYBX88XXprotein

213 - - - - - - - - - P T L N P E T V A I N L - - - S D V D L S K Y I T T I A G V M h Fas protein
318 Y Q G A D P I L A T A L A S D P I P N P L Q K W E D S A H K P Q S L D T D D P A h TNFR I Protein
305 S R A L G P A A A P T L S P - - - - - - - - - - E S P A G S P A M M L Q P G P Q DR3 protein
283 - - - - - - - - - - - L E P A E A E R S Q R R R L L V P A N E G D P T E T L R Q HLYBX88XXprotein
```

FIG.2B

```
241 T L S Q V - - - - - - - - - K G F V R K N G V N E A K I D E I K N D N V Q D T A  h Fas protein
358 T L Y A V V E N V P P L R W K E F V R R L G L S D H E I D R L E L Q N G R C L R  h TNFR I Protein
335 - L Y D V M D A V P A R R W K E F V R T L G L R E A E I E A V E V E I G R - F R  DR3 protein
312 C F D D F A D L V P F D S W E P L M R K L G L M D N E I - K V A K A E A A G H R  HLYBX88XXprotein

272 E Q K V Q L L R N W H Q L H G K K E A - Y D T L I K D L K K A N L C T L A E K I  h Fas protein
398 E A Q Y S M L A T W R R R T P R R E A T L E L L G R V L R D M D L L G C L E D I  h TNFR I Protein
373 D Q Q Y E M L K R W R Q Q Q P - - - A G L G A V Y A A L E R M G L D G C V E D L  DR3 protein
351 D T L Y T M L I K W V N K T G R - D A S V H T L L D A L E T L G E R L A K Q K I  HLYBX88XXprotein

311 Q T I I L K D I T S D S E N S N F R N E I Q S L V                                 h Fas protein
438 E E A L - - - - - - - C G P A A L P P A P S L L R                                 h TNFR I Protein
410 - - - - - - - - - - - - - R S R L Q R G P                                         DR3 protein
390 E D H L L S S G K F M Y L E G N - - A D S A M S                                   HLYBX88XXprotein
```

FIG.2C

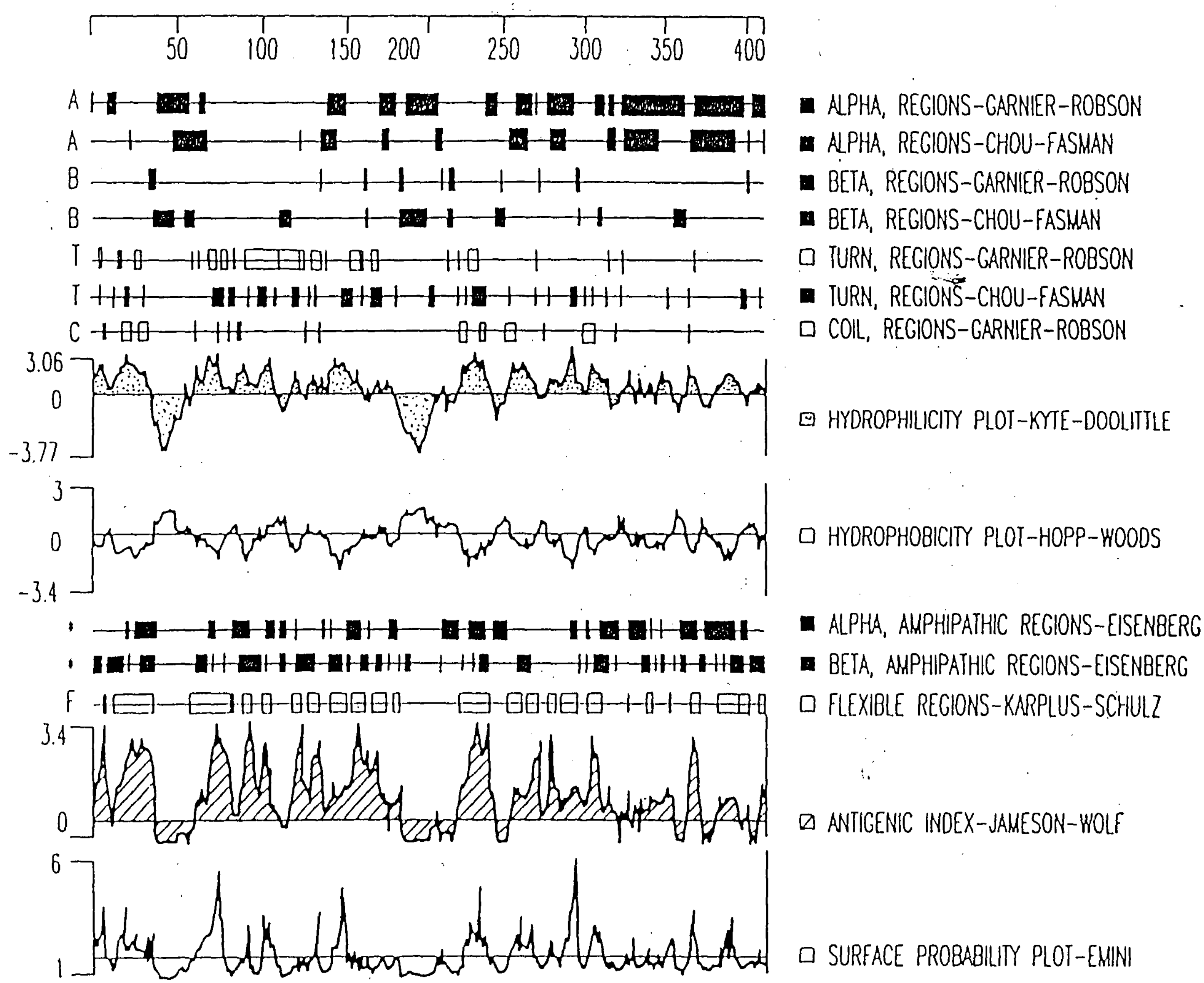

50
100
150
200
250
300
350
400
A
A
B
B
T
T
C
3.06
0
-3.77
3
0
-3.4
F
3.4
0
6
1
ALPHA, REGIONS-GARNIER-ROBSON
ALPHA, REGIONS-CHOU-FASMAN
BETA, REGIONS-GARNIER-ROBSON
BETA, REGIONS-CHOU-FASMAN
TURN, REGIONS-GARNIER-ROBSON
TURN, REGIONS-CHOU-FASMAN
COIL, REGIONS-GARNIER-ROBSON
HYDROPHILICITY PLOT-KYTE-DOOLITTLE
HYDROPHOBICITY PLOT-HOPP-WOODS
ALPHA, AMPHIPATHIC REGIONS-EISENBERG
BETA, AMPHIPATHIC REGIONS-EISENBERG
FLEXIBLE REGIONS-KARPLUS-SCHULZ
ANTIGENIC INDEX-JAMESON-WOLF
SURFACE PROBABILITY PLOT-EMINI

FIG.3

```
HAPBU13R
  1 AATTCGGCAC AGCTCTTCAG GAAGTCAGAC CTTCCCTGGT TTACCTTTTT
 51 TCTGGAAAAA GCCCAACTGG GACTCCAGTC AGTAGGAAAG TGCCACAATT
101 GTCACATGAC CGGTACTGGA AGAAACTCTC CCATCCAACA TCACCCAGTG
151 GNATGGGAAC ACTGATGAAC TTTTCACTGC ACTTGGCATT ATTTTTGTNA
201 AGCTGAATGT GATAATAAGG GCACTGATGG AAATGTCTGG ATCATTCCGG
251 TTGTGCGTAC TTTGAGATTT GNGTTTGGGG ATGTNCATTG TGTTTGACAG
301 CACTTTTTTN ATCCCTAATG TNAAATGCNT NATTTGATTG TGANTTGGGG
351 GTNAACATTG GTNAAGGNTN CCCNTNTGAC ACAGTAGNTG GTNCCCGACT
401 TANAATNGNN GAANANGATG NATNANGAAC CTTTTTTTGG GTGGGGGGGT
451 NNCGGGGCAG TNNAANGNNG NCTCCCCAGG TTTGGNGTNG CAATNGNGGA
501 ANNNTGG

HSBBU76R
  1 TTTTTTTTGT AGATGGATCT TACAATGTAG CCCAAATAAA TAAATAAAGC
 51 ATTTACATTA GGATAAAAAA GTGCTGTGAA AACAATGACA TCCCAAACCA
101 AATCTCAAAG TACGCACAAA CGGAATGATC CAGACATTTC CATAGNGTCC
151 TTATTATCAC ATTCAGCTTA TAAAANTAAT GCCAAGTGCA GTGAAAAGTT
201 ACAGGATGTT CCATCCACTG GGTGGATT
```

FIG.4

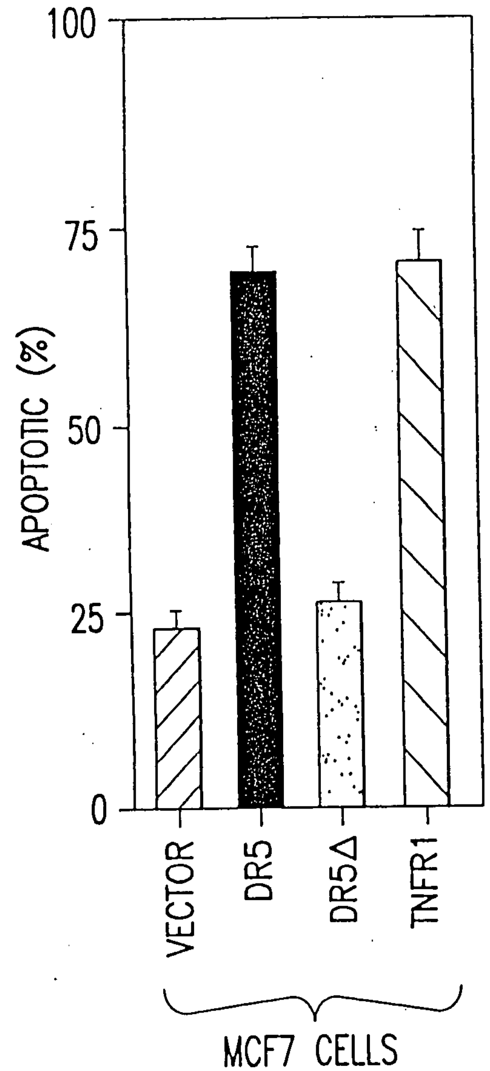



FIG. 5A

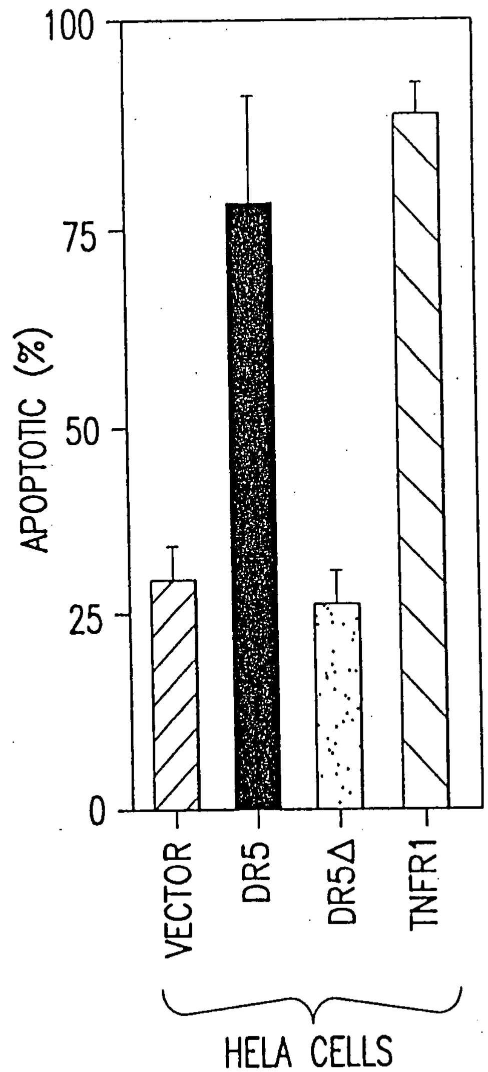



FIG. 5B

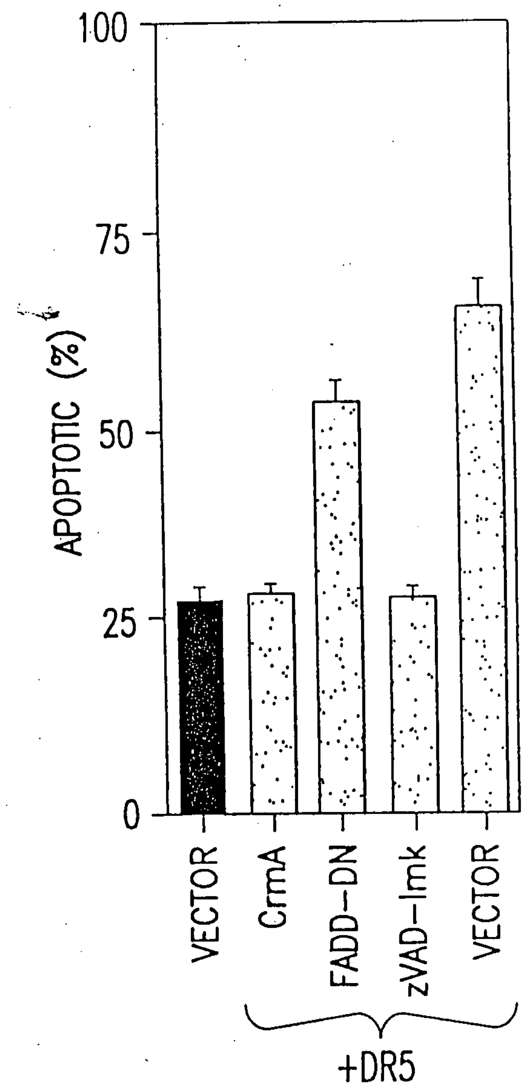



FIG. 5C

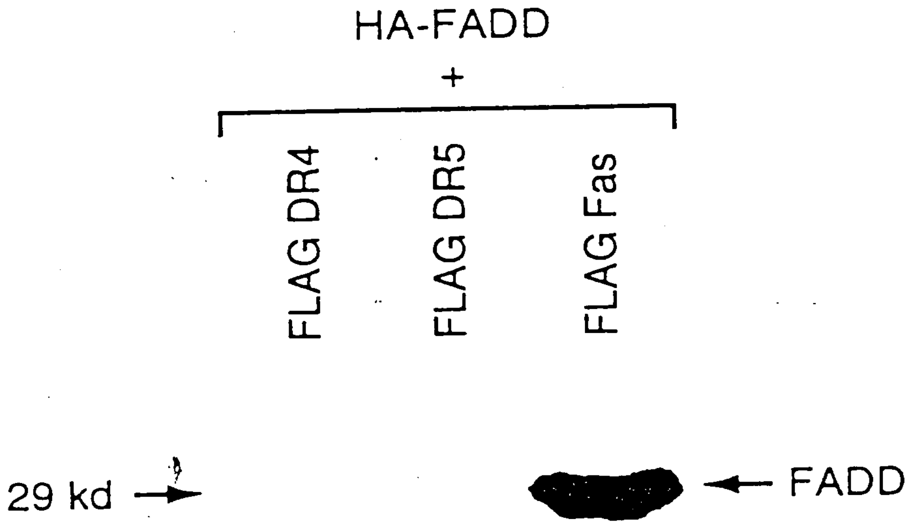
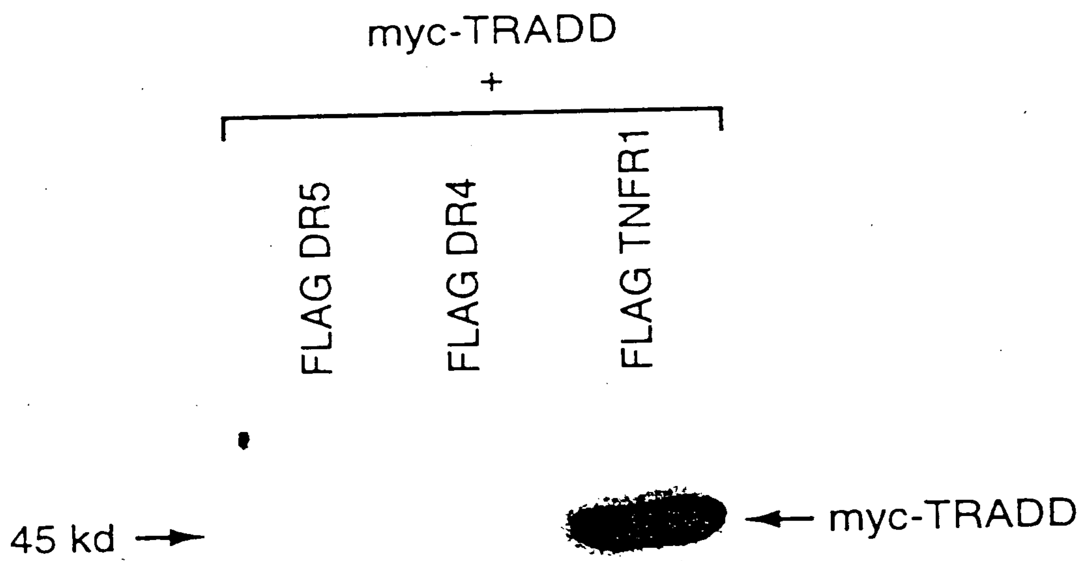
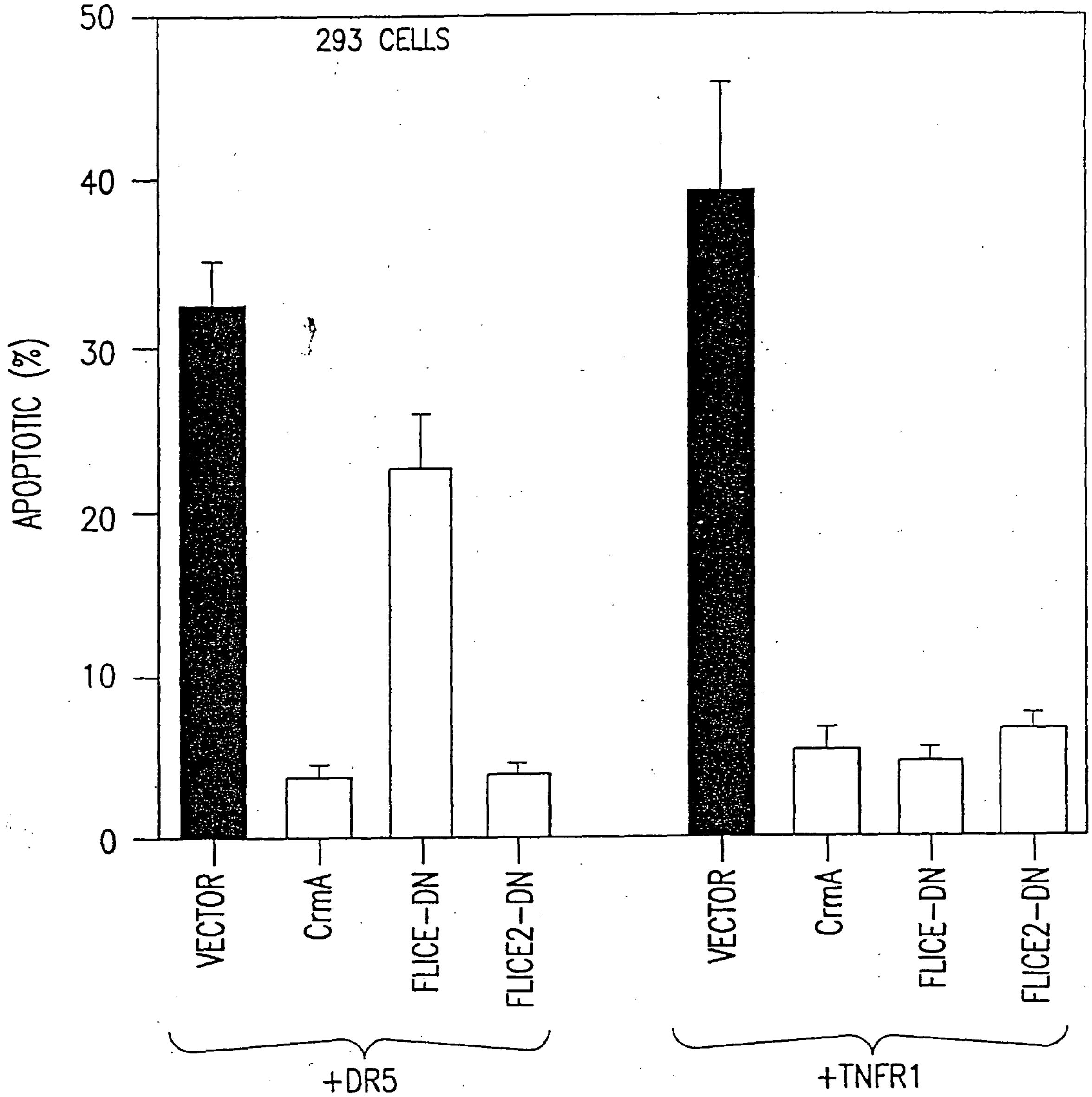

HA-FADD
+
FLAG DR4
FLAG DR5
FLAG Fas
29 kd
FADD

FIG.5D


myc-TRADD
+
FLAG DR5
FLAG DR4
FLAG TNFR1
45 kd
myc-TRADD



50
40
30
20
10
0
APOPTOTIC (%)
293 CELLS
VECTOR
CrmA
FLICE-DN
FLICE2-DN
VECTOR
CrmA
FLICE-DN
FLICE2-DN
+DR5
+TNFR1


FIG. 5E

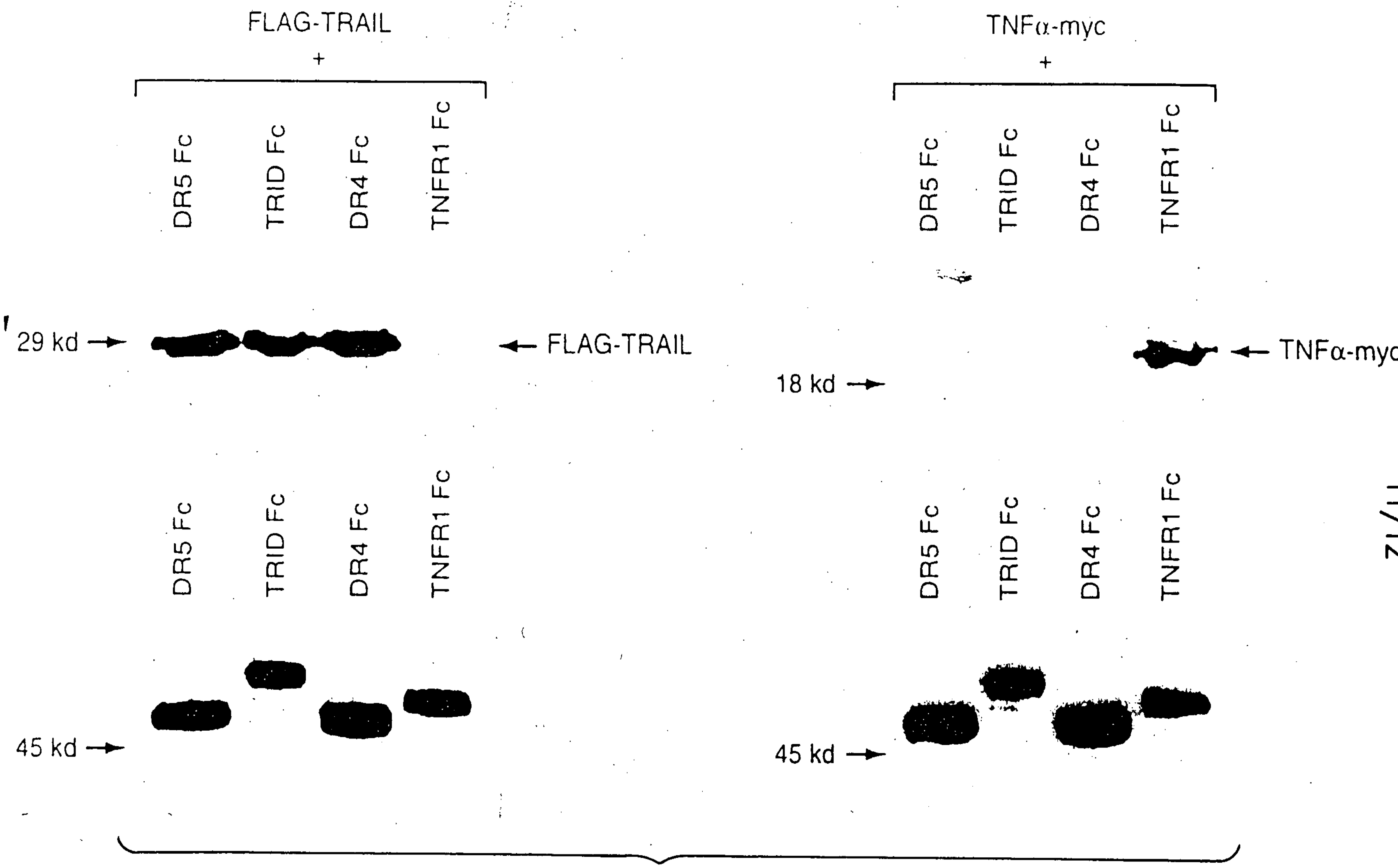

FLAG-TRAIL
+
DR5 Fc
TRID Fc
DR4 Fc
TNFR1 Fc
29 kd
FLAG-TRAIL
DR5 Fc
TRID Fc
DR4 Fc
TNFR1 Fc
45 kd
TNFα-myc
+
DR5 Fc
TRID Fc
DR4 Fc
TNFR1 Fc
18 kd
TNFα-myc
DR5 Fc
TRID Fc
DR4 Fc
TNFR1 Fc
45 kd

FIG.6A

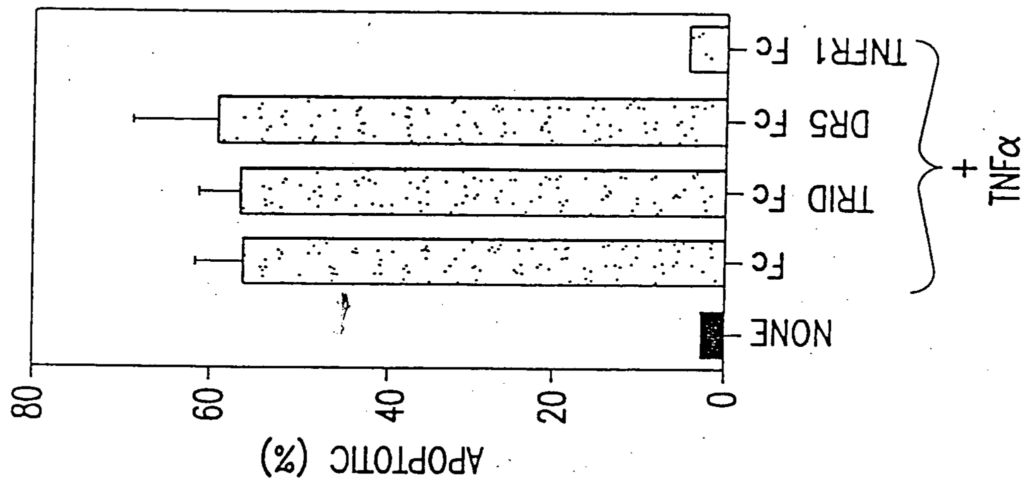

APOPTOTIC (%)
80
60
40
20
0
NONE
Fc
TRID Fc
DR5 Fc
TNFR1 Fc
+
TNFα

FIG. 6C

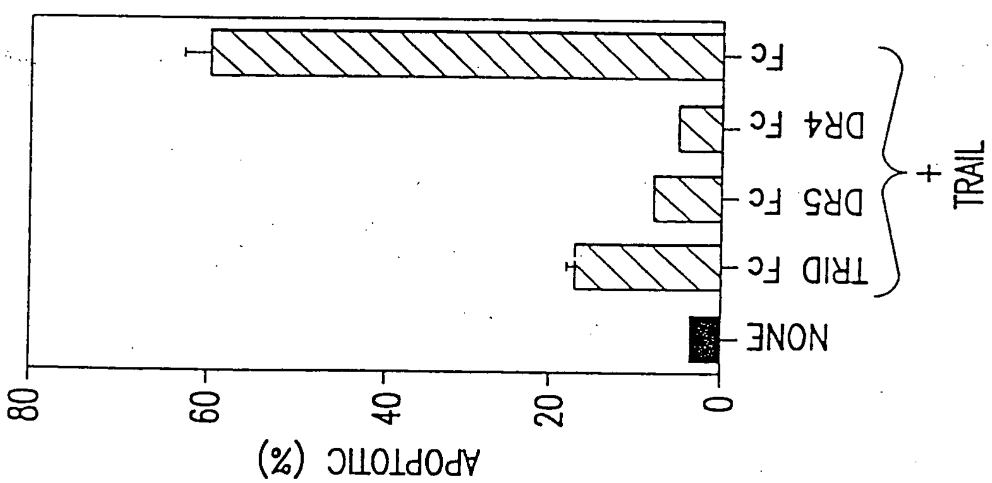

APOPTOTIC (%)
80
60
40
20
0
NONE
TRID Fc
DR5 Fc
DR4 Fc
Fc
+
TRAIL

FIG. 6B